

APPENDIX F  
Application 10/782,435  
Docket 1121C RuvB

GAP comparison of sequences in WO 2004/003013 application.

Polynucleotides – Percent Sequence Identity

SEQ ID	CQ760237	CQ760239	CQ760241
1	72.694	52.193	51.695
3	72.767	52.852	52.119
5	72.767	52.281	51.342
7	72.840	52.535	51.412
9	73.152	50.797	51.133

Polypeptides – Percent Sequence Identity

SEQ ID	CQ760237aa	CQ760239aa	CQ760241aa
2	84.615	45.946	44.965
4	85.055	45.946	44.965
6	85.275	45.270	44.836
8	85.275	45.495	44.836
10	85.388	45.902	45.122

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GAP of: CQ760237 check: 1467 from: 1 to: 1377

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WPDEF 1121 RuvB NCBI CQ760237 from WO2004/00313
1121 RuvB NCBI CQ760237 from WO2004/00313
LOCUS      CQ760237      1377 bp      DNA      linear      PAT 17-APR-2005
DEFINITION Sequence 4 from Patent WO2004003013.
ACCESSION  CQ760237
VERSION    CQ760237.1  GI:44903794 . . .

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to: 1121SID3 check: 4044 from: 1 to: 1912

WPDEF Case 1121 SEQ ID NO: 3 RuvB

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	10020	Length:	1912
Ratio:	7.277	Gaps:	0
Percent Similarity:	72.767	Percent Identity:	72.767

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 5
. = 1
```

1121CQ760237 x 1121SID3      October 4, 2005 17:43      ..

1 .....atgggagaaagtaaaga 16  
51 ctccacagaaacagagagcgcataaccggcgcgcttggcggcgatgagga 100  
17 ttgaagaaattcagtcaccgcctaagaaacaacggattgctactcacacc 66  
101 tcgaggaggtgcagtcgacctcgaagaagcagcgcacatcgccacccacacc 150  
67 catatcaaaggccttggcctcgagccaactggatatccctataaaattggc 116  
151 cacatcaagggactcggcctcgacgccaatgggatggcgattgcgttggc 200  
117 agctggattttgttgggtcaacttgaggctagagaggcagctggtcttgtag 166  
201 ggcggggttcgtggggccaggcgggcgcgcgaggcgggccgggctggcgg 250  
167 ttgacatgattaagcagaagaaaatggcggggcaaggctcttttgcttgct 216  
251 tcgacatgattcgccagaagaagatggccgggccgcgcggtgctccttgcg 300

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```
217 ggacctcctggaactgggaaaacagctttggctcttggaatctctcaaga 266
    || || || || || || || || || || || || || || || || ||
301 ggtccgcccgcacgggcaagacggcgctagcgctcggcatagcccagga 350

267 gctgggaagcaagggtccattctgtccaatgggttgatctgaggtttact 316
    || || || || || || || || || || || || || || || || ||
351 gctcggcagcaagggtccctttctgtcctatggtaggatcagaagtgtact 400

317 catcagagggttaagaaaacagagggttctcatggagaatttttagacgtgcc 366
    | | | | | | | | | | | | | | | | | | | | | | | |
401 cctcggagggtcaagaaaactgagggtgctgatggaaaatttccgtagagct 450

367 attgggtctacgtatcaaggaaaccaaagaagtctatgaaggggaggtcac 416
    || || || || || || || || || || || || || || || || ||
451 atagggtttgcgtataaaggaaaacaaagagggttatgaaggagaggttac 500

417 cgagctgtcaccagaagaaactgaaagcctcactggagggttatggtaaaa 466
    || || || || || || || || || || || || || || || || ||
501 tgaactttccccagaagaggctgagagtacaactgggtggatatgcaaaaa 550

467 gcatcagccatgttgtaattacactcaagacagtcaaaggaaccaaacat 516
    || || || || || || || || || || || || || || || || ||
551 gcattagccatgtaatcatcagcttaaagactgttaaagggactaagcaa 600

517 ctgaaattggatcccactatctatgatgccttgattaaggaaaaggtagc 566
    || || || || || || || || || || || || || || || || ||
601 ctgaagttagattcttcaatttatgatgctctgatcaaggaaaaggtagc 650

567 tgtaggagatgtaatctatatcgaagcaaacagtggagctgtcaaacggg 616
    || || || || || || || || || || || || || || || || ||
651 agtgggtgatgttatatacatcgaagcaaatagtggagcagtgaaaagag 700

617 taggtagaagtgatgcttttgccactgaatttgatctggaagcagaagaa 666
    | | | | | | | | | | | | | | | | | | | | | | | |
701 ttggtagatgtgattcttttgctacagaatacgatcttgaagctgaagag 750

667 tatgttccacttcccaaaggagagggtccacaaaaagaaagagatagtgc 716
    || || || || || || || || || || || || || || || || ||
751 tatgttcctatcccaaagggtgaagtcataagaaaaaagaaattgtgca 800

717 ggatgtcacactccaagatctggatgcagcaaagtctcgacctcaagggtg 766
    || || || || || || || || || || || || || || || || ||
801 ggatgtcacacttcatgaccttgatgcagcaaagtctcagccacaagggtg 850

767 gccaggatatactttctttgatgggccaaatgatgaaaccgcggaagact 816
    || || || || || || || || || || || || || || || || ||
851 gccaaagatattttgtcccttatgggccagatgatgaaaccacgaaagact 900

817 gagatcactgataagcttcggcaagaaattaacaagggttgtgaaccgata 866
    || || || || || || || || || || || || || || || || ||
901 gaaatcaccgaaaaactacgccaagaaattaataagggtggtaaatagata 950
```

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867	tatagatgaaggtgtggcagagcttgttccaggagtctattttatttgatg	916
951	tatcgatgaaggaattgcagagcttgtagctgtttgttcatttgatg	1000
	.	
917	aggttcataatgcttgatattggagtgcttctcatacttgaaccgtgctctt	966
1001	aggtccacatgtttggatatcgaatgtttttcttatcttaaccgtgcattg	1050
	.	
967	gagagctcattatctccgatagtgatatttgcaacaaatagagggtgtttg	1016
1051	gagagcccattatcaccaatcgtgatacttgctacaaatagggggaatatg	1100
	.	
1017	caacgtaagaggggactgatatgccagcccccatggagtccttattgatc	1066
1101	taatgtaagaggaactgatatgacaagtccacatgggtataccgggtggatc	1150
	.	
1067	tattagatcgatttggttatcatccggactcaaattctatgatccctctgaa	1116
1151	ttctagataggctgggtgattattcggacagagacatatggccctactgag	1200
	.	
1117	atgatccagattatagccattcgtgcgcaagttgaagaattaaccgtgga	1166
1201	atgatacagatatattggctatccgagcacaagtgaggaggagattgatatgga	1250
	.	
1167	tgaagaatgcttggttctacttggggagattggggcaagaacttcactaa	1216
1251	tgaagaaagtcttgcttattttaggcgagatcggacagcagacatctttga	1300
	.	
1217	ggcacgctgtgcagcttctgtctcctgccagcattgtagcgaataatgaat	1266
1301	gacatgctatttcaattgatatcacctgccagcgtgggtctcaaagactaat	1350
	.	
1267	ggcctgacaaatatttgcaaggctgatatagaggaagtaaacatcactcta	1316
1351	ggaagagagaaaatctgcaaggctgatctcgaggaagtcagtgggctcta	1400
	.	
1317	cttggtatgctaaatcttcagcaaaagcttttgcgatgagcaacaagaaaaat	1366
1401	tttggtatgccaaatcctcgggtcgggtgctccaggagcaacaagaaagat	1450
	.	
1367	acatctcatga.....	1377
1451	acatcacctagattttgqatctcctgtcgtggaagtctcgaagagaatgta	1500

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GAP of: CQ760237aa check: 5361 from: 1 to: 458

WPDEF 1121 RuvB NCBI encoded by CQ760237 from WO2004/00313

1121 RuvB NCBI encoded by CQ760237 from WO2004/00313

SEQ ID NO: 5 NCBI CAF32893

LOCUS CQ760237 1377 bp DNA linear PAT 17-APR-2005

DEFINITION Sequence 4 from Patent WO2004003013.

ACCESSION CQ760237 . . .

to: 1121SID4 check: 8436 from: 1 to: 455

WPDEF Case 1121 SEQ ID NO: 4 RuvB

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl.  
Acad.

Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	1994	Length:	458
Ratio:	4.382	Gaps:	0
Percent Similarity:	90.110	Percent Identity:	85.055

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

1121CQ760237aa x 1121SID4 October 4, 2005 18:01 ..

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      .
1 MEKVKIEEIQSTAKKQRIATHTHIKGLGLEPTGIPIKLAAGFVGQLEARE 50
      .:||||:||||.|||||||||||||||||:|. |||
1 ...MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAARE 47
      .
51 AAGLVVDMIKQKKMAGKALLLAGPPGTGKTALALGISQELGSKVPFCPMV 100
      |||||:||||:|.||||| |||
48 AAGLAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMV 97
      .
101 GSEVYSSEVKKTEVLMENFRAIGLRIKETKEVYEGEVTELSPEETESLT 150
      |||
98 GSEVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGEVTELSPEEAESTT 147
      .
151 GGYGKSISHVVITLKTVMGTHLKLDPITYDALIKEKVAVGDVIYIEANS 200
      ||| |||||:|.||||| ||| .|||||
148 GGYAKSISHVIISLKTVMGTHLKLDPITYDALIKEKVAVGDVIYIEANS 197
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```
201 GAVKRVGRSDAFATEFDLEAEYVPLPKGEVHKKKEIVQDVTLQDLDAAN 250
    ||||| |. |||: |||||: ||||| |||||
198 GAVKRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAAN 247

251 ARPQGGQDILSLMGQMMKPRKTEITDKLRQEINKVNNRYIDEGVAELVPG 300
    |. |||||: |||||: |||||: |||||
248 AQPGGGQDILSLMGQMMKPRKTEITEKLRQEINKVNNRYIDEGIAELVPG 297

301 VLFIDEVHMLDMECFSYLNRALESSLSPIVIFATNRGVCNVRGTDMPSPH 350
    ||||| |. ||||| ||||| |||||: ||||| |||
298 VLFIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPH 347

351 GVPIDLLDRLVIIRTQIYDPSEMIQIIAIRAQVEELTVDEECLVLLGEIG 400
    |: |: ||||| |||||: | |. |||||: |||||: . ||| | |||||
348 GIPVDLLDRLVIIRTETYGPTEMIQILAIRAQVEEIDMDEESLAYLGEIG 397

401 QRTSLRHAVQLLSPASIVAKMNGRDNICKADIEEVTSLYLDAKSSAKLLH 450
    |. |||||: |: |||||: |. | |||: |||||: |||. ||||| |||||: |||
398 QQTSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQ 447

451 EQQEKYIS 458
    ||||: ||.
448 EQQERYIT 455
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